

## ALIGNMENT #4

Qy	368 HisGlnLysGlyLysAspGluGlyValValTyrSerValValHisArgThrSerLysArg 387
Ds	1081 CACCGAAAGGGAAAGATGAAGGTGTTGCTACTCTGTGGTCATAGAACCTCAAAGAGG 1140
Qy	388 SerGluAlaArgSerAlaGluPheThrValGlyArgLysAspSerSerIleIleCysAla 407
Ds	1141 AGTGAAGCCAGGCTCTGCTGAGTCAACCGTGGGAGAACGACAGTTCTATCATCTGTGGC 1200
Qy	408 GluValArgCysLeuGlnProSerGluValSerSerThrGluValAsnMetArgSerArg 427
Ds	1201 GAGGTGAGATGCCCTGCAGCCCCAGTGAGGTTCATCCACGGAGGTGAATAATGAGAACAGG 1260
Qy	428 ThrLeuGlnGluProLeuSerAspCysGluGluValLeuCys 441
Ds	1261 ACTCTCCAAGAACCCCTTAGCCACTGTGAGGAGTTCTCTGC 1302

## RESULT 5

DJ447641

LOCUS DJ447641 1997 bp DNA linear PAT 10-JUL-2008  
 DEFINITION A novel immunosuppressive receptor.  
 ACCESSION DJ447641  
 VERSION DJ447641.1 GI:194091312  
 KEYWORDS JP 2004208583-A/2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
     Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
     Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1997)  
 AUTHORS Takahashi,T., Manabe,T., Isogai,T., Sugiyama,T., Irie,R.,  
     Wakamatsu,A., Ishii,S. and Sato,H.  
 TITLE A novel immunosuppressive receptor  
 JOURNAL Patent: JP 2004208583-A 2 29-JUL-2004;  
     Mochida Pharmaceutical Co Ltd, Research Association for  
     Biotechnology  
 COMMENT OS homo sapiens  
     PN JP 2004208583-A/2  
     PD 29-JUL-2004  
     PF 27-DEC-2002 JP 2002381558  
     PI tomohiro takahashi,tadashi manabe,takao isogai,tomoyasu PI  
     sugiyama,  
     PI ryotaro irie,ai wakamatsu,shizuko ishii,hiroyuki sato CC  
     FH Key Location/Qualifiers.  
 FEATURES Location/Qualifiers  
 source 1..1997  
     /organism="Homo sapiens"  
     /mol\_type="unassigned DNA"  
     /db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Length:	1997	Matches:	438
Score:	2302.00	Conservative:	1
Percent Similarity:	99.3%	Mismatches:	0
Best Local Similarity:	99.1%	Indels:	3
Query Match:	98.4%	Gaps:	1
DB:	9		

US-10-574-045-4 (1-441) x DJ447641 (1-1997)

Qy	1 MetLeuProSerLeuGlyProMetLeuLeuTrpThrAlaValLeuLeuPheValProCys 20 
Db	87 ATGTGCCATCTTAGGCCCATGCTCTGACGGCTGTGCTGCTCTTGTCCCTGT 146
Qy	21 ValGlyLysThrValTrpLeuTyrLeuGlnAlaTrpProAsnProValPheGluGlyAsp 40 
Db	147 GTTGGGAAACTGTCTGGCTGTACCTCCAAGCCTGGCAAACCCCTGTGTTGAAGGAGAT 206
Qy	41 AlaLeuThrLeuArgCysGlnGlyTrpLysAsnThrProLeuSerGlnValLysPheTyr 60 
Db	207 GCCCCGACTCTGCGATGTCAAGGGATGGAAGAATCACCACTGTCTCAGGTGAAGTTCTAC 266
Qy	61 ArgAspGlyLysPheLeuHisPheSerLysGluAsnGlnThrLeuSerMetGlyAlaAla 80 
Db	267 AGAGATGGAAAATTCTTCATTTCTCTAAGGAAAACCAGACTCTGTCATGGGAGCAGCA 326
Qy	81 ThrValGlnSerArgGlyGlnTyrSerCysSerGlyGlnValMetTyrIleProGlnThr 100 
Db	327 ACAGTCAGAGCCGTGGCAGTACAGCTGCTCTGGCAGGTGATGTATATTCCACAGACA 386
Qy	101 PheThrGlnThrSerGluThrAlaMetValGlnValGlnGluIeuPheProProProVal 120 
Db	387 TTACACACAAACTTCAGAGACTGCGCATGGTCAGCTCAAGAGCTGTITCCACCTCTGTG 446
Qy	121 LeuSerAlaIleProSerProGluProArgGluGlySerLeuValThrLeuArgCysGln 140 
Db	447 CTGAGTGCCATCCCCTCTCTGAGCCCCGAGAGGGTAGCCTGGTACCCCTGAGATGTCAG 506
Qy	141 ThrLysLeuHisProLeuArgSerAlaLeuArgLeuLeuPheSerPheHisLysAspGly 160 
Db	507 ACAAGCTGCACCCCCCTGAGGTCAAGCTTCTGAGGCTCTTCTCCACAAGGACGGC 566
Qy	161 HisThrLeuGlnAspArgGlyProHisProGluLeuCysIleProGlyAlaLysGluGly 180 
Db	567 CACACCTTGCGGACAGGGCCCTCACCCAGAACCTGCGATCCGGAGCCAAAGGAGGGA 626
Qy	181 AspSerGlyLeuTyrTrpCysGluValAlaProGluGlyGlyGlnValLysGlnSer 200 
Db	627 GACTCTGGGCTTACTGGCTGAGGTGGCCCCCTGAGGGTGGCCAGGTCAGAACAGAGC 686
Qy	201 ProGlnLeuGluValArgValGlnAlaProValSerArgProValLeuThrLeuHisHis 220 
Db	687 CCCACGCTGGAGTCAGAGTGCAGGCTCTGTATCCGTCCTGTGCTACTCTGCACAC 746

Qy	221 GlyProAlaAspProAlaValGlyAspMetValGlnLeuLeuCysGluAlaGlnArgGly 240 
Ds	747 GGGCCTGCCTGACCCCTGCTGTGGGGGACATGGTGCAGGTCCTCTGTGAGGGCACAGGGGGC 806
Qy	241 SerProProIleLeuTyrSerPheTyrLeuAspGluLysIleValGlyAsnHisSerAla 260 
Ds	807 TCCCCCTCCGATCTGTATTCCTCTACCTTGATGAGAACATTGTGGGAACCAACTCAGCT 866
Qy	261 ProCysGlyGlyThrThrSerLeuLeuPheProValLysSerGluGlnAspAlaGlyAsn 280 
Ds	867 CCCTGTGGTGAACCACTCCCTCTCTTCCCAGTGAAGTCAGAACAGGGATGCTGGGAAC 926
Qy	281 TyrSerCysGluAlaGluAsnSerValSerArgGluArgSerGluProLysLysLeuSer 300 
Ds	927 TACTCTGCGAGGCTGAGAACAGTGTCTCCAGAGAGAGGAGTGAGCCAAGAAGCTGTCT 986
Qy	301 LeuLysGlySerGlnValLeuPheThrProAlaSerAsnTrpLeuValProTrpLeuPrc 320 
Ds	987 CTGAAGGGTTCTCAAGTCTGGTCACTCCGCCAGCAACTGGCTGGTCTGGCTTC 1046
Qy	321 AlaSerLeuLeuGlyLeuMetValIleAlaAlaAlaLeuLeuValTyrValArgSerTrp 340 
Ds	1047 GCGAGGCTGCTGGCTGATGGTTATTGCTGTCAGTCTGGTTATGTGAGATCCTGG 1106
Qy	341 ArgLysAlaGlyProLeuProSerGlnIleProProThrAlaProGlyGluGlnCys 360 
Ds	1107 AGAAAAGCTGGGCCCTCCATCCCAGATAACCACCCACAGCTCCAGGTGGAGAGCAGTGC 1166
Qy	361 ProLeuTyrAlaAsnValHisHisGlnLysGlyLysAspGluGlyValValTyrSerVal 380 
Ds	1167 CCACTATATGCCAACGTGCATCACCGAGAAAGGAAAGATGAAGGTGTGTACTCTGTG 1226
Qy	381 ValHisArgThrSerLysArgSerGluAlaArgSerAlaGluPheThrVal-TyrSerVal 400 
Ds	1227 GTGCATAGAACCTCAAAGAGGAGTGAAGGCCAGTGTGAGTTACCGTGCCCC----- 1281
Qy	400 sAspSerSerIleIleCysAlaGluValArgCysLeuGlnProSerGluValSerSerTh 420 :::
Ds	1282 -GAAAGTTCTATCATCTGCGGAGGTGAGATGCCAGTGAGTTACCGTGCCCC----- 1340
Qy	420 rGluValAsnMetArgSerArgThrLeuGlnGluProLeuSerAspCysGluGluValLe 440 
Ds	1341 GGAGGTGAAATATGAGAACAGGACTCTCCAAGAACCCCTTAGCGACTGTGAGGAGCTCT 1400
Qy	440 uCys 441 
Ds	1401 CTGC 1404

#### RESULT 6

AK131201

LOCUS AK131201

1997 bp mRNA linear PRI 09-JAN-2008